BIOTECI LOGY

#### RAW SEQUENCE LISTING ERROR REPORT



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The Blotechnology Systems Branch of the Scientific and Technic 11.

Center (STIC) detected errors when processing the following computer is unabled to fine.

Application Serial Number: 09/530-209

Source: 163

THE STATE OF STREET

Date Processed by STIC: 2/21/20

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER

To and the second control of the second

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R: Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R: Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

#### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the art Windows based software programs employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old nules) and the revised version (new rules) effective July 1, 1998 as well as World Intelligent (WIPO) Standard ST.25

compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

1638

PAGE: 1

46

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:22

INPUT SET: S36432.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

se pp. 6-7

	1 2	SEQUENCE LISTING	Does Not Comply Corrected Diskette Needed
	3	(1) General Information:	Paragram Signature Meeded
>	4 5 6 7	(i) APPLICANT: 1 mort up - all responses must (A) NAME+ CropDesign NV	t be on same line as heading
>	8	(B) STREET: TechnologiePark Zwijnaarde 3	_
>	9	(D) STATE: none	
> >	10	(E) COUNTRY: Belgium	
>	11	(F) POSTAL CODE (ZIP): 9052	
,	12	/ (F) FOSTRE CODE (BIT) 1-5002	
	13 14	(ii) TITLE OF INVENTION: A novel mitogenic cyclin	
	15	(iii) NUMBER OF SEQUENCES: 4	SPONDENCE ADDRESS: add there DORESSEE: MEET: MY: ATE: UNTRY: Leadings and
	16	(IV) CURKE	SPONDENCE ADDRESS: DORESSEE:
	17	(V) (iv) COMPUTER READABLE FORM: (6) ST	mandatory
	18	(A) MEDIUM TVDE, Florov diek (Dist.	ATE:
	19	(B) COMPUTER: IBM PC compatible © ZP	UNTRY: fladings and
	20	(C) OPERATING SYSTEM: PC-DOS/MS-DOS	
	21	(D) SOFTWARE: PatentIn Release #1.0, Version	#1.30 ((EPO)) responses for
	22	A .	#1.30 (EPO) responses for a U.S. case
	23	(NO CURRENT APPLICATION DATA: WAS APPLICATION NUMBER: Cold mardatory Leadings	a dis.
	24	(B) FILING DATE:	$\Psi$
	25	(2) INFORMATION FOR SEQ ID NO: 1:	THE CALL
	26		ri invalid for a U.S. case
	27	(i) SEQUENCE CHARACTERISTICS:	
	28	(A) LENGTH: 927 base pairs	invalid Co
	29	(B) TYPE: nucleic acid	12 mulla fora
	30	(C) STRANDEDNESS: double	
	31	(D) TOPOLOGY: linear	7/ ( )
	32		U.S. Case
	33	(ii) MOLECULE TYPE: cDNA	
	34		
	35	(iii) HYPOTHETICAL: NO	
	36		
	37	(ix) FEATURE:	
	38	(A) NAME/KEY: CDS	
	39	(B) LOCATION:1927	
	40		
	41	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
	42		
	43	ATG GCA GAG GAA AAT CTA GAA CTG AGT CTT TTA TGT ACA GAG	
	44	Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu	ı Ser Asn
	45	1 6 10	16

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:22

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47	GTT	GAT	GAT	GAG	GGC	ATG	ATT	GTT	GAC	GAA	ACT	CCG	ATT				96
48	Val	Asp	Asp	Glu	Gly	Met	Ile	Val	Asp	Glu	Thr	Pro	Ile	Glu	Ile	Ser	
49		_	_	20	_				25					30			
50																	
51	ATT	CCT	CAG	ATG	GGT	TTT	TCT	CAA	TCG	GAG	AGT	GAG	GAG	ATT	ATC	ATG	144
52	Ile	Pro	Gln	Met	Gly	Phe	Ser	Gln	Ser	Glu	Ser	Glu	Glu	Ile	Ile	Met	
53			35					40					45				
54																	
55	GAG	ATG	GTG	GAG	AAG	GAG	AAG	CAG	CAT	TTG	CCA	AGT	GAT	GAT	TAC	ATC	192
56	Glu	Met	Val	Glu	Lys	Glu	Lys	Gln	His	Leu	Pro	Ser	Asp	Asp	Tyr	Ile	
57		50					55					60	•				
58																	
59												GTT					240
60	-	Arg	Leu	Arg	Ser	_	Asp	Leu	Asp	Leu		Val	Gly	Arg	Arg	_	
61	65					70					75					80	
62		`									~	~- ~				~~-	
63												CAC					288
64	Ala	ьeu	Asn	Trp		Trp	ьys	Ala	Cys		vaı	His	GIN	Pne	_	Pro	
65					85					90				•	95		•
66	mm/C	mcm	<b></b>	TICC	תיווי א	CCA	איזייר	7 7 C	መአሮ	TTTC	CAT	CGA	TTC	תיתי א	TOC	CITION	336
67 68												Arg					
69	пец	Cys	FIIC	100	цец	лта	Met	MOII	105	·	тэр	Arg	FIIC	110	DCI	val	
70				100					103					110			
71	САТ	GAT	ттG	ССТ	AGT	GGC	ΑΑΑ	GGT	TGG	ΑΤΑ	TTG	CAG	TTG	TTG	GCT	GTG	384
72												Gln					001
73		<u>-</u>	115				-1-	120					125				
74																	
75	GCT	TGT	TTA	TCA	TTG	GCA	GCC	AAA	ATT	GAA	GAA	ACT	GAA	GTT	CCA	ATG	432
76	Ala	Cys	Leu	Ser	Leu	Ala	Ala	Lys	Ile	Glu	Glu	Thr	Glu	Val	Pro	Met	
77		130					135	_				140					
78																	
79	TTG	ATA	GAT	CTT	CAG	GTT	GGA	GAT	CCT	CAG	TTT	GŢG	TTT	GAG	GCT	AAA	480
80	Leu	Ile	Asp	Leu	Gln	Val	Gly	Asp	Pro	Gln	Phe	Val	Phe	Glu	Ala	Lys	
81	145					150					155					160	
82																	
83												AAA					528
84	Ser	Val	GIn	Arg		Glu	Leu	Leu	Val		Asn	Lys	Leu	Lys	-	Arg	
85					165					170					175		
86 87	mmc	707	CCA	א מיזי א	λCIT	007	шсс	TICI N	ma C	אידות	202	TAT	mmc	CMC	202	220	57 <i>6</i>
88												Tyr					576
89	пеп	Arg	Ala	180	1111	PIO	Cys	Ser	185	116	Arg	ıyı	FILE	190	ALG	nys	
90				100					103					170			
91	ATG	AGT	AAA	TGT	GAT	CAA	GAA	CCA	TCC	AAC	ACA	TTG	АТА	тст	AGA	TCA	624
92												Leu					024
93			195	-1-				200					205		5		
94			<b>-</b>														
95	TTA	CAA	GTG	ATA	GCC	AGC	ACA	ACC	AAA	GGT	ATT	GAC	TTT	TTG	GAG	TTT	672
96	Leu	Gln	Val	Ile	Ala	Ser	Thr	Thr	Lys	Gly	Ile	Asp	Phe	Leu	Glu	Phe	
97		210					215		_	_		220					
98																	
99	AGA	CCT	TCT	GAA	GCT	GCT	GCT	GCT	GTG	GCA	CTT	TCT	GTT	TCT	GGA	GAA	720

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:23

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100	Arg	Pro	Ser	Glu	Ala	Ala	Ala	Ala	Val	Ala	Leu	Ser	Val			_	
101	225					230					235					240	
102																	
103	TTG	CAG	AGA	GTA	CAC	TTT	GAC	AAC	TCT	TCC	TTC	TCT	CCT	CTT	TTC	TCA	768
104	Leu	Gln	Arg	Val	His	Phe	Asp	Asn	Ser	Ser	Phe	Ser	Pro	Leu	Phe	Ser	
105			_		245		-			250					255		
106																	
107	CTA	CTT	CAA	AAG	GAG	AGA	GTG	AAG	AAG	ATA	GGG	GAA	ATG	ATA	GAG	AGT	816
108	Leu	Leu	Gln	Lys	Glu	Arg	Val	Lys	Lys	Ile	Gly	Glu	Met	Ile	Glu	Ser	
109				260					265					270			
110																	
111																GTA	864
112	Asp	Gly	Ser	Asp	Leu	Cys	Ser	Gln	Thr	Pro	Asn	Gly	Val	Leu	Glu	Val	
113			275					280					285				
114																	
115	TCG	GCT	TGT	TGT	TTC	AGC	TTT	AAG	ACC	CAT	GAT	TCT	TCT	TCT	TCT	TAT	912
116	Ser	Ala	Cys	Cys	Phe	Ser	Phe	Lys	Thr	His	Asp	Ser	Ser	Ser	Ser	Tyr	
117		290					295					300					
118																	
119	ACA	CAT	CTT	TCT	TAA												927
120	Thr	His	Leu	Ser	*												
121	305													:			
122																	
123																	
124	(2)	INF	ORMA!	rion	FOR	SEQ	ID I	10: 3	2:								
125																	
126				-			RACTI										
127			(2	A) LI	ENGTI	1: :	308 a	amino	o ac:	ids							
120			•	•													
128			(1	B) T	YPE:		no a										•
129			(1	B) T	YPE:		no ao line										•
129 130			(1	B) T? D) T(	PE: OPOLO	GY:	line	ear									•
129 130 131			1) 1) 10M (	B) TY D) TO LECUI	(PE: OPOLO	OGY:	line	ear cein	7.00	rD 11/							
129 130 131 132			1) 1) 10M (	B) TY D) TO LECUI	(PE: OPOLO	OGY:	line	ear cein	SEQ I	ID NO	D: 2:	:					·
129 130 131 132 133	Mah	(xi)	(I (I ) MOI ) SE(	B) TY D) TO LECUI	(PE: OPOLO LE TY	OGY: VPE: ESCRI	line prot	ear tein DN: 8					mb ~	Cl.,	Con	ħ a n	·
129 130 131 132 133 134		(xi)	(I (I ) MOI ) SE(	B) TY D) TO LECUI	(PE: OPOLO LE TY CE DI Asn	OGY: VPE: ESCRI	line	ear tein DN: 8		Leu			Thr	Glu		Asn	·
129 130 131 132 133 134 135	Met 1	(xi)	(I (I ) MOI ) SE(	B) TY D) TO LECUI	(PE: OPOLO LE TY	OGY: VPE: ESCRI	line prot	ear tein DN: 8					Thr	Glu	Ser 15	Asn	·
129 130 131 132 133 134 135 136	1	(xi)	(I (I ) MOI ) SEG	B) TY D) TO LECUI QUENO Glu	YPE: DPOLO LE TY CE DI Asn 5	OGY: (PE: ESCR: Leu	line prot IPTIC	ear cein ON: S	Ser	Leu 10	Leu	Cys			15		
129 130 131 132 133 134 135 136	1	(xi)	(I (I ) MOI ) SEG	B) TY D) TO LECUI QUENO Glu Glu	YPE: DPOLO LE TY CE DI Asn 5	OGY: (PE: ESCR: Leu	line prot	ear cein ON: S	Ser Asp	Leu 10	Leu	Cys		Glu	15		
129 130 131 132 133 134 135 136 137	1	(xi)	(I (I ) MOI ) SEG	B) TY D) TO LECUI QUENO Glu	YPE: DPOLO LE TY CE DI Asn 5	OGY: (PE: ESCR: Leu	line prot IPTIC	ear cein ON: S	Ser	Leu 10	Leu	Cys			15		
129 130 131 132 133 134 135 136 137 138	1 Val	(xi) Ala Asp	(I (I ) MOI ) SE( Glu Asp	B) TY D) TO LECUI QUENC Glu Glu 20	YPE: DPOLO LE TY CE DI Asn 5	OGY: /PE: ESCRI Leu Met	line prot IPTIC Glu Ile	ear cein ON: S Leu Val	Ser Asp 25	Leu 10 Glu	Leu Thr	Cys Pro	Ile	Glu 30	15 Ile	Ser	
129 130 131 132 133 134 135 136 137 138 139 140	1 Val	(xi) Ala Asp	(I (I ) MOI ) SE( Glu Asp	B) TY D) TO LECUI QUENC Glu Glu 20	YPE: DPOLO LE TY CE DI Asn 5	OGY: /PE: ESCRI Leu Met	line prot IPTIC	ear cein DN: S Leu Val	Ser Asp 25	Leu 10 Glu	Leu Thr	Cys Pro	Ile Glu	Glu 30	15 Ile	Ser	
129 130 131 132 133 134 135 136 137 138 139 140	1 Val	(xi) Ala Asp	(I (I ) MOI ) SE( Glu Asp	B) TY D) TO LECUI QUENC Glu Glu 20	YPE: DPOLO LE TY CE DI Asn 5	OGY: /PE: ESCRI Leu Met	line prot IPTIC Glu Ile	ear cein ON: S Leu Val	Ser Asp 25	Leu 10 Glu	Leu Thr	Cys Pro	Ile	Glu 30	15 Ile	Ser	
129 130 131 132 133 134 135 136 137 138 139 140 141	1 Val Ile	(xi) Ala Asp Pro	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met	YPE: DPOLO LE TY CE DE Asn 5 Gly	OGY: YPE: ESCRI Leu Met Phe	prot PTIC Glu Ile Ser	cear cein DN: S Leu Val	Ser Asp 25 Ser	Leu 10 Glu Glu	Leu Thr Ser	Cys Pro Glu	Ile Glu 45	Glu 30 Ile	15 Ile Ile	Ser Met	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	1 Val Ile	(xi) Ala Asp Pro	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met	PE: DPOLO LE TY CE DE Asn 5 Gly	OGY: YPE: ESCRI Leu Met Phe	prot prot Glu Ile Ser	cear cein DN: S Leu Val	Ser Asp 25 Ser	Leu 10 Glu Glu	Leu Thr Ser	Cys Pro Glu Ser	Ile Glu 45	Glu 30 Ile	15 Ile Ile	Ser Met	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	1 Val Ile	(xi) Ala Asp Pro	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met	PE: DPOLO LE TY CE DE Asn 5 Gly	OGY: YPE: ESCRI Leu Met Phe	prot PTIC Glu Ile Ser	cear cein DN: S Leu Val	Ser Asp 25 Ser	Leu 10 Glu Glu	Leu Thr Ser	Cys Pro Glu	Ile Glu 45	Glu 30 Ile	15 Ile Ile	Ser Met	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	1 Val Ile Glu	(xi) Ala Asp Pro Met 50	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENO Glu Glu 20 Met	PE: DPOLO LE TY CE DE Asn 5 Gly Gly	OGY:  VPE: ESCRI  Leu  Met  Phe  Glu	prot IPTIC Glu Ile Ser Lys 55	cear cein DN: S Leu Val Gln 40	Ser Asp 25 Ser	Leu 10 Glu Glu Leu	Leu Thr Ser Pro	Cys Pro Glu Ser 60	Ile Glu 45 Asp	Glu 30 Ile Asp	15 Ile Ile Tyr	Ser Met Ile	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	1 Val Ile Glu Lys	(xi) Ala Asp Pro Met 50	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENO Glu Glu 20 Met	PE: DPOLO LE TY CE DE Asn 5 Gly Gly	OGY:  VPE: ESCRI  Leu  Met  Phe  Glu  Gly	prot prot Glu Ile Ser	cear cein DN: S Leu Val Gln 40	Ser Asp 25 Ser	Leu 10 Glu Glu Leu	Leu Thr Ser Pro	Cys Pro Glu Ser 60	Ile Glu 45 Asp	Glu 30 Ile Asp	15 Ile Ile Tyr	Ser Met Ile	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146	1 Val Ile Glu	(xi) Ala Asp Pro Met 50	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENO Glu Glu 20 Met	PE: DPOLO LE TY CE DE Asn 5 Gly Gly	OGY:  VPE: ESCRI  Leu  Met  Phe  Glu	prot IPTIC Glu Ile Ser Lys 55	cear cein DN: S Leu Val Gln 40	Ser Asp 25 Ser	Leu 10 Glu Glu Leu	Leu Thr Ser Pro	Cys Pro Glu Ser 60	Ile Glu 45 Asp	Glu 30 Ile Asp	15 Ile Ile Tyr	Ser Met Ile	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	Val Ile Glu Lys 65	(xi) Ala Asp Pro Met 50 Arg	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met Glu Arg	PE: DPOLO LE TY CE DE Asn 5 Gly Gly Lys Ser	Phe Glu Gly 70	prot prot Glu Ile Ser Lys 55	cear cein DN: S Leu Val Gln 40 Gln Leu	Ser Asp 25 Ser His	Leu 10 Glu Glu Leu	Leu Thr Ser Pro Asn 75	Cys Pro Glu Ser 60 Val	Ile Glu 45 Asp Gly	Glu 30 Ile Asp	15 Ile Ile Tyr Arg	Ser Met Ile Asp 80	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	Val Ile Glu Lys 65	(xi) Ala Asp Pro Met 50 Arg	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met Glu Arg	PE: DPOLO LE TY CE DE Asn S Gly Gly Lys Ser	Phe Glu Gly 70	prot IPTIC Glu Ile Ser Lys 55	cear cein DN: S Leu Val Gln 40 Gln Leu	Ser Asp 25 Ser His	Leu 10 Glu Glu Leu Leu	Leu Thr Ser Pro Asn 75	Cys Pro Glu Ser 60 Val	Ile Glu 45 Asp Gly	Glu 30 Ile Asp	15 Ile Ile Tyr Arg	Ser Met Ile Asp 80	
129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	Val Ile Glu Lys 65	(xi) Ala Asp Pro Met 50 Arg	(I (I) (I) (I) (I) (I) (I) (I) (I) (I) (	B) TY D) TO LECUI QUENC Glu Glu 20 Met Glu Arg	PE: DPOLO LE TY CE DE Asn 5 Gly Gly Lys Ser	Phe Glu Gly 70	prot prot Glu Ile Ser Lys 55	cear cein DN: S Leu Val Gln 40 Gln Leu	Ser Asp 25 Ser His	Leu 10 Glu Glu Leu	Leu Thr Ser Pro Asn 75	Cys Pro Glu Ser 60 Val	Ile Glu 45 Asp Gly	Glu 30 Ile Asp	15 Ile Ile Tyr Arg	Ser Met Ile Asp 80	

204

205

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:23

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														<i>I</i> ?	<b>VPUT</b>	SET:	S36432.raw
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154																	
155	His	Asp		Pro	Ser	Gly	Lys	_	Trp	Ile	Leu	Gln		Leu	Ala	Val	
156			115					120					125				
157		_		_	_												
158	Ala	_	Leu	Ser	Leu	Ala		Lys	Ile	Glu	Glu		Glu	Val	Pro	Met	
159		130					135					140					
160	7	T7.	7	T	a1	17_ 7	<b>a</b> 1	3	D	<b>~1</b>	Db -	11- 7	Dla a	<b>~</b> 1	. 1 -	<b>T</b>	
161 162	145	116	Asp	ьeu	Gln	150	GIY	Asp	Pro	GIII		vaı	Pne	GIU	Ald	_	
162	143					150					155					160	
164	Ser	Va 1	Gln	Δνα	Met	Glu	T. <del>2</del> 11	T. <del>2</del> 11	Va 1	T. <del>2</del> 11	Δen	Laze	T.e.11	Lvc	Trn	Ara	
165	DCI	Vai	GIII	arg	165	GIU	DCu	БСи	Val	170	ASII	ny s	LCu	цуз	175	A+ 9	
166										_,,							
167	Leu	Arq	Ala	Ile	Thr	Pro	Cvs	Ser	Tvr	Ile	Arq	Tvr	Phe	Leu	Arq	Lvs	
168		J		180			- 2		185			- 2		190		<b>2</b>	
169																	
170	Met	Ser	Lys	Cys	Asp	Gln	Glu	Pro	Ser	Asn	Thr	Leu	Ile	Ser	Arg	Ser	
171			195					200					205				
172																	
173	Leu		Val	Ile	Ala	Ser		Thr	Lys	Gly	Ile	-	Phe	Leu	Glu	Phe	
174		210					215					220					
175	•	_		<b>~</b> 1					7			_	1		<b>~</b> 1	<b>~</b> 1	
176		Pro	ser	GIU	Ala		Ата	Ата	vaı	Ата		ser	vai	ser	GIY		
177 178	225					230					235					240	
179	Len	Gln	Δra	Val	His	Phe	Asn	Δsn	Ser	Ser	Phe	Ser	Pro	T.e.11	Phe	Ser	
180	LCu	0111	**-9	vul	245		пор	71011	501	250	1110	501	110	Leu	255	501	
181																	
182	Leu	Leu	Gln	Lys	Glu	Arg	Val	Lys	Lys	Ile	Gly	Glu	Met	Ile	Glu	Ser	
183				260		_		-	265		_			270			
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186			275					280					285				
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188	ser		Cys	Cys	Phe	ser		Lys	Thr	His	Asp		Ser	Ser	Ser	Tyr	
189 190		290					295					300					
190	Thr	uic	Leu	Sar													
192	305	птэ	пец	SEL													
193	303																
194																	
195	(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10: 3	}:								
196																	
197		(i)		-	CE CF		TERI	STIC	cs:								
198					ENGTH		24		5.								
199				-	PE:												
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201			(I	) TC	POLC	GY:	line	ar									
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203		(11)	MOL	ILCOT	E TY	PE:	otne	r nu	стел	.c ac	πα						

(A) DESCRIPTION: /desc = "oligonucleotide"

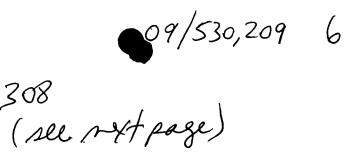
# RAW SEQUENCE LISTING PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:23

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208	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
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210	GAACACTCGA GTGTAATGGC AGAGG	25
211		
212		
213	•	
214	(2) INFORMATION FOR SEQ ID NO: 4:	
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216	(i) SEQUENCE CHARACTERISTICS:	
217	(A) LENGTH: 25	
218	(B) TYPE: nucleic acid	
219	(C) STRANDEDNESS: single	
220	(D) TOPOLOGY: linear	
221		
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223	(A) DESCRIPTION: /desc = "oligonucleotide	, II
224		_
225	(iii) HYPOTHETICAL: YES	
226		
227	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
228		
229	CATCATACTA GTTATAATAA TGTAAG	26
230		

#### (2) INFORMATION FOR SEQ ID-



· (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 369 amino acids 308

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Glu Glu Asn Leu Glu Leu Ser Leu Leu Cys Thr Glu Ser Asn 1 15

Val Asp Asp Glu Gly Met Ile Val Asp Glu Thr Pro Ile Glu Ile Ser

Ile Pro Gln Met Gly Phe Ser Gln Ser Glu Ser Glu Ile Ile Met

Glu Met Val Glu Lys Glu Lys Gln His Leu Pro Ser Asp Asp Tyr Ile

Lys Arg Leu Arg Ser Gly Asp Leu Asp Leu Asn Val Gly Arg Arg Asp

Ala Leu Asn Trp Ile Trp Lys Ala Cys Glu Val His Gln Phe Gly Pro 90

Leu Cys Phe Cys Leu Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Val 105

His Asp Leu Pro Ser Gly Lys Gly Trp Ile Leu Gln Leu Leu Ala Val 115

Ala Cys Leu Ser Leu Ala Ala Lys Ile Glu Glu Thr Glu Val Pro Met

Leu Ile Asp Leu Gln Val Gly Asp Pro Gln Phe Val Phe Glu Ala Lys 150 155 160

Ser Val Gln Arq Met Glu Leu Leu Val Leu Asn Lys Leu Lys Trp Arq 165 170

Leu Arg Ala Ile Thr Pro Cys Ser Tyr Ile Arg Tyr Phe Leu Arg Lys 180 185

Met Ser Lys Cys Asp Gln Glu Pro Ser Asn Thr Leu Ile Ser Arg Ser 195 200

Leu Gln Val Ile Ala Ser Thr Thr Lys Gly Ile Asp Phe Leu Glu Phe 215

Arg Pro Ser Glu Ala Ala Ala Val Ala Leu Ser Val Ser Gly Glu 225 235

Leu Gln Arg Val His Phe Asp Asn Ser Ser Phe Ser Pro Leu Phe Ser 245 250

Leu Leu Gln Lys Glu Arg Val Lys Lys Ile Gly Glu Met Ile Glu Ser 260 265 270

9

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Asp Gly Ser Asp Leu Cys Ser Gln Thr Pro Asn Gly Val Leu Glu Val 275 280 285

Ser Ala Cys Cys Phe Ser Phe Lys Thr His Asp Ser Ser Ser Ser Tyr 290 295 300

Thr His Leu Ser (\*)

Delete erdig stop codon

#### SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:24

INPUT SET: S36432.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: CropDesign NV
7	Unknown or Misplaced Identifier	(B) STREET: TechnologiePark Zwijnaarde 3
8	Unknown or Misplaced Identifier	(C) CITY: Gent
9	Unknown or Misplaced Identifier	(D) STATE: none
10	Unknown or Misplaced Identifier	(E) COUNTRY: Belgium
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 9052
195	Stop Codon at end of sequence removed - no error	(2) INFORMATION FOR SEQ ID NO: 3:

# SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/09/530,209

DATE: 02/27/2001 TIME: 20:20:24

INPUT SET: S36432.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
CURRENT APPLICATION DATA
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA